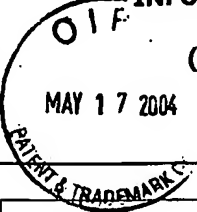


FORM PTO-1449 LIST OF PATENTS AND OTHER ITEMS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT (Use several sheets if necessary) MAY 17 2004 	ATTY. DOCKET NO. 01561.0002.CNUS03	SERIAL NO. <u>10/777829</u>
	APPLICANT: Arnold J. Mandell, et al.	
	FILING DATE: 2/11/04	GROUP: <u>N/A 1631</u>

U.S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
			None			

FOREIGN PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	TRANSLATION YES NO
			None			

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, etc.)

<i>Duplicate</i>	AA	Mandell, A.J. (1984) Non-equilibrium behavior of some brain enzyme and receptor systems. Ann. Rev. Pharm. Toxicol. 24:237-274
<i>123</i>	AB	Mandell, A.J., Russo, P.V. and Blomgren, B.W. (1987) Complex hydrophobic sequence transformation predicts mutual recognition by polypeptides and proteins. Ann. N.Y. Acad. Sci. 504:88-118.
<i>Duplicate</i>	AC	Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Mode matches and their locations in the hydrophobic free energy sequences of peptide ligands and their receptor eigenfunctions. Proc. Natl. Acad. Sci. 94:13576-13581.
<i>Duplicate</i>	AD	Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Wavelet transformation of protein hydrophobicity sequences suggests their memberships in structural families. Physica A224: 254-262.

EXAMINER: <i>J.B. Bruce 18 February 2007</i>	DATE CONSIDERED: <i>18 February 2007</i>
EXAMINER: Initial if reference is considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include a copy of this form with next communication to applicant	

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Duplicate	AE	Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1997) Hydrophobic free energy eigenfunctions help define continuous wavelet transformations of amino acid sequences of protein families. Proc. Intl. (Fermi) Sch. Phys. CXXXIV, 175-192.
Duplicate	AF	Di-Marzo, E.A. and Mandell, A.J. (1997) Phase transition behavior of a linear macromolecule threading a membrane. J. Chem. Physics 107:5510-5514.
Duplicate	AG	Mandell, A.J., Owens, M.I., Selz, K.A., Morgan, W.N., Schlesinger, M.F. and Nemeroff, C.G. (1998) Mode matches in hydrophobic free energy eigenfunctions predict protein-protein interactions. Biopolymers 46:89-101.
Duplicate	AH	Selz, K.A., Mandell, A.J., and Shlesinger, M.F. (1998) Hydrophobic free energy eigenfunctions of pore, channel and transporter proteins contain B-burst patterns. Biophysical J. 75:2332-2342.
BB	AI	Mandell, A.J., Selz, K.A. and Shlesinger, M.F. (1998) Transformational homologies in amino acid sequences suggest membership in protein families. J. Stat. Phys. 93:673-697.
Duplicate	AJ	Mandell, A.J., Selz, K.A., Shlesinger, M.F., and Kuhar, M.J. (1999) Linear and entropic transformations of the hydrophobic free energy sequence help characterize a novel brain polypeptide: CART. In (M.T. Batchelor and L. Wille, eds.), Statistical Physics on the Eve of the Twenty-First Century. World Scientific, NJ, pp. 131-152.
BB	AK	Manavalan, P. and Ponnuswamy, P.K. (1978) Statistical distribution of hydrophobic residues along the length of protein chains, Biophys. J., Volume 57 pp. 911-921. White et al. 1990
BB	AL	White, Stephen H. and Jacobs, Russell E. (1994) Global Statistics of Protein Sequences: Implications for the Origin, Evolution, and Prediction of Structure. Annu. Rev. Biophys. Biomol. Struct. 23:407-439.
Duplicate	AM	Doyle, P.M. (1995) Combinatorial Chemistry in the Discovery and Development of Drugs. J. Chem. Tech. Biotechnol. 64:317-324.
Duplicate	AN	Gordon, E.M., Barrett, R.W., Dower, W.J., Fodor, S.P.A. and Gallop, M.A. (1994) Applications of Combinatorial Technologies to Drug Discovery. 2. Combinatorial Organic Synthesis, Library Screening Strategies, and Future Directions. J. Med. Chem. 37(10):1385-1401.
Duplicate	AO	Houghton, R.A. (1993) The Broad Utility of Soluble Peptide Libraries for Drug Discovery. Gene 137:7-11.

SD-84546.1

EXAMINER: Examiner <i>J.B. Bruce</i>	DATE CONSIDERED: <i>18 February 2007</i>
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<i>duplicate</i>	AP	Mandell, Arnold J., Selz, Karen A., and Shlesinger, Michael F. Predicting Peptide – Receptor, Peptide- Protein, and Chaperone-Protein Binding using patterns in amino acid hydrophobic free energy sequences, The Journal of Physical Chemistry B, Vol 104, No. 16, pgs 3953-3959
<i>JB</i>	AQ	Chorev M. et al. "Recent Developments in Retro Peptides and Proteins – An Ongoing Topochemical Exploration", Trends in Biotechnology, Elsevier, Amsterdam, NL., vol. 13, no. 10, October 1995 (1995-10), pages 438-445, XP004207219 ISSN: 0167-7799
<i>JB</i>	AR	RAFFA: "Drug-Receptor Thermodynamics: Introduction and Applicatons," May 2001 (2001-05), John Wiley & Sons XP001153602. Mandell et al: Hydrophobic Mode-Targeted, Algorithmically Designed Peptide Ligands Structure as Modulators of Protein Thermodynamic Structure and Function page 655-page 700

SD-84546.1

EXAMINER: Examiner <i>John S. Brusca</i>	DATE CONSIDERED: <i>18 February 2007</i>
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